

Editorial on Cannabis Genome Current Trends

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Cannabis sativa L., a native plant of Central Asia, is first cultivated in Asia and Europe and is now one of the most popularly cultivated plants worldwide. In China, hemp fiber has been used to produce textiles for the past 6000 years.

C. sativa is one of the most valuable agriculturally important crops in nature. Although it is widely used to produce paper, textiles, building materials, food, and medicine, a secondary metabolite, tetrahydrocannabinol (THC), is also used to produce well-known drugs. Frequent, long-term, selective breeding has produced both hemp fiber and medicinal cannabis strains, with medicinal cannabis showing promise in effectively treating various diseases by relieving an array of symptoms, including pain, nausea, anxiety, and inflammation. The therapeutic efficacy of medicinal cannabis is mainly dependent on cannabinoids, which are endemic metabolites unique to *C. sativa*, among which THC and cannabidiol (CBD) are the main chemical cannabinoid compounds.

The cannabis genome has been sequenced, but the sequenced plant came from a cultivated variety. Generally, cultivated varieties lose substantial genetic diversity through successive bottlenecks due to domestication and selection for traits to increase yield under intensive

human cultivation. Therefore, wild-type varieties are an important source of genetic diversity for molecular breeding. In this report, we performed genomic sequencing, assembly, annotation, and evolutionary analysis in wild-type varieties of *C. sativa*. The genetic data obtained in this study will be a valuable resource for future studies assessing the pharmacology, chemical constituents, cultivation, and genetic improvement of the traits of these plants and could be used as a reference in future population genetic studies of *C. sativa*.

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